fasterq_dump output → runs/{s}/{s}_1.fastq runs/{s}/{s}_2.fastq cat_runids_to_samples input <input function> <input function> output → samples/{samid,SAMN[0-9]{6,9}}_1.fastq

gzip

samples/ $\{$ samid, $SAMN[0-9]\{6,9\}\}_2$.fastq

→ input

samples/{samid}_1.fastq
samples/{samid}_2.fastq

output →

samples/{samid,SAMN[0-9]{6,9}}_1.fastq.gz
samples/{samid,SAMN[0-9]{6,9}}_2.fastq.gz

download_remote

output →

refs/downloads/{f}

extract_genome

→ input

refs/downloads/GRCh38.d1.vd1.fa.tar.gz

output →

refs/sequences/genome.dict
refs/sequences/genome.fa.gz
refs/sequences/genome.fa.gz.fai

star_index

→ input

refs/downloads/gencode.v38.annotation.gtf.gz
refs/sequences/genome.fa.gz

output →

refs/index.star/genome

telescope_annotation

→ input

refs/downloads/retro.hg38.v1.gtf
refs/sequences/genome.fa.gz.fai

output →

refs/annotation/retro.gtf

star_alignment

→ input

refs/index.star/genome
samples/{samid}_1.fastq.gz
samples/{samid}_2.fastq.gz

output →

results/star_alignment/{samid,SAMN[0-9]{6,9}}/{samid}_GDC38.Aligned.out.bam

telescope

→ input

refs/annotation/retro.gtf

 $results/star_alignment/\{samid\}/\{samid\}_GDC38.Aligned.out.bam$

output →

 $results/telescope/\{samid,SAMN[0-9]\{6,9\}\}/\{samid\}-telescope_report.tsv$

sample_complete

→ input

results/telescope/{samid}/{samid}-telescope_report.tsv

output →

results/completed/{samid,SAMN[0-9]{6,9}}_completed.txt

all

→ input

results/completed/SAMN13178814_completed.txt results/completed/SAMN13178815_completed.txt results/completed/SAMN13178816_completed.txt results/completed/SAMN13178817 completed.txt results/completed/SAMN13178818_completed.txt results/completed/SAMN13178819_completed.txt results/completed/SAMN13178820_completed.txt results/completed/SAMN13178821_completed.txt results/completed/SAMN13178822_completed.txt results/completed/SAMN13178823_completed.txt results/completed/SAMN13178824_completed.txt results/completed/SAMN13178825_completed.txt results/completed/SAMN13178826_completed.txt results/completed/SAMN13178827_completed.txt results/completed/SAMN13178828_completed.txt results/completed/SAMN13178829_completed.txt results/completed/SAMN13178830_completed.txt